A

Fully
Folded

$i = 0$

Partition
1

$i = 1$ $i = 2$ $i = 144$ $. . . .i = 2,046$

Partition
2

$i = 2,047$ $i = 2,048$ $i = 2,190$ $. . . .i = 4,092$

Partition
5

$i = 7,161$ $i = 7,162$ $i = 7,314$ $. . . .i = 9,207$

Fully
Unfolded

$i = 9,208$

Figure 1A

B

$$\Delta ASA = (ASA_{unfolded\ unit} + ASA_{complimentary}) - (ASA_{native\ unit})$$

Ser 26

Asp 27
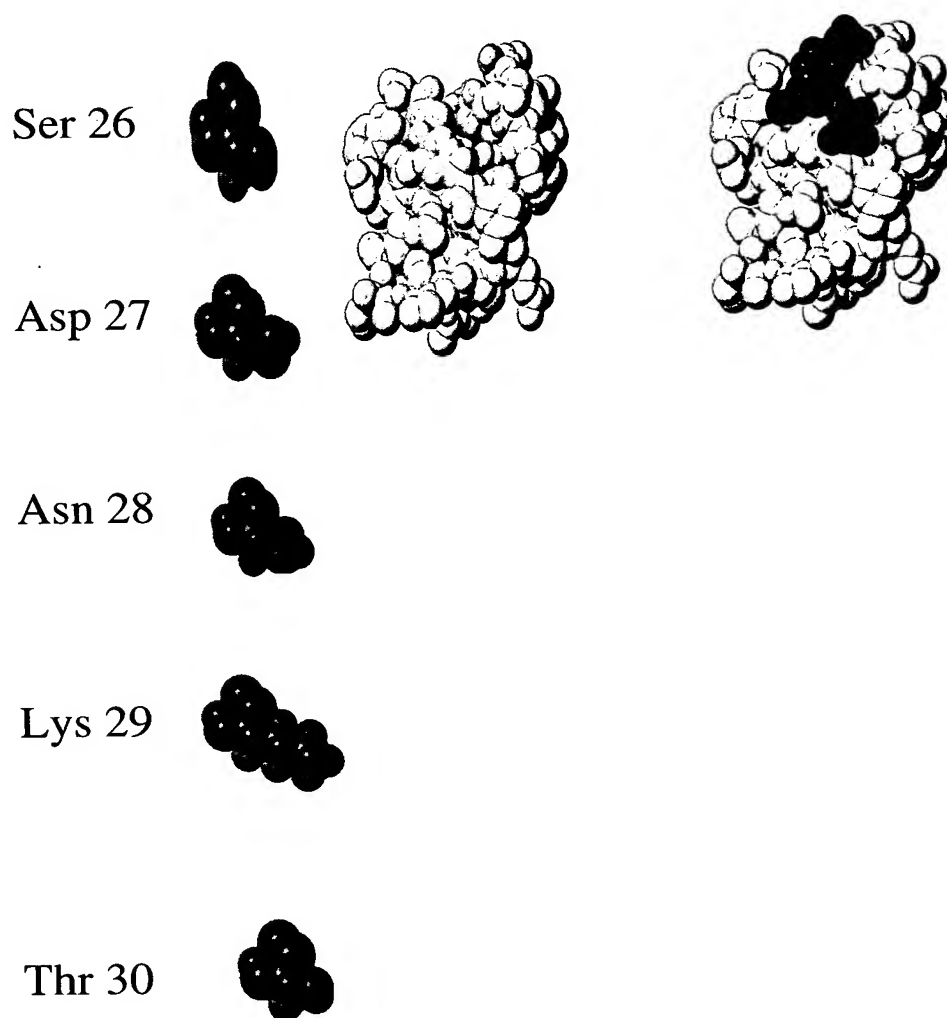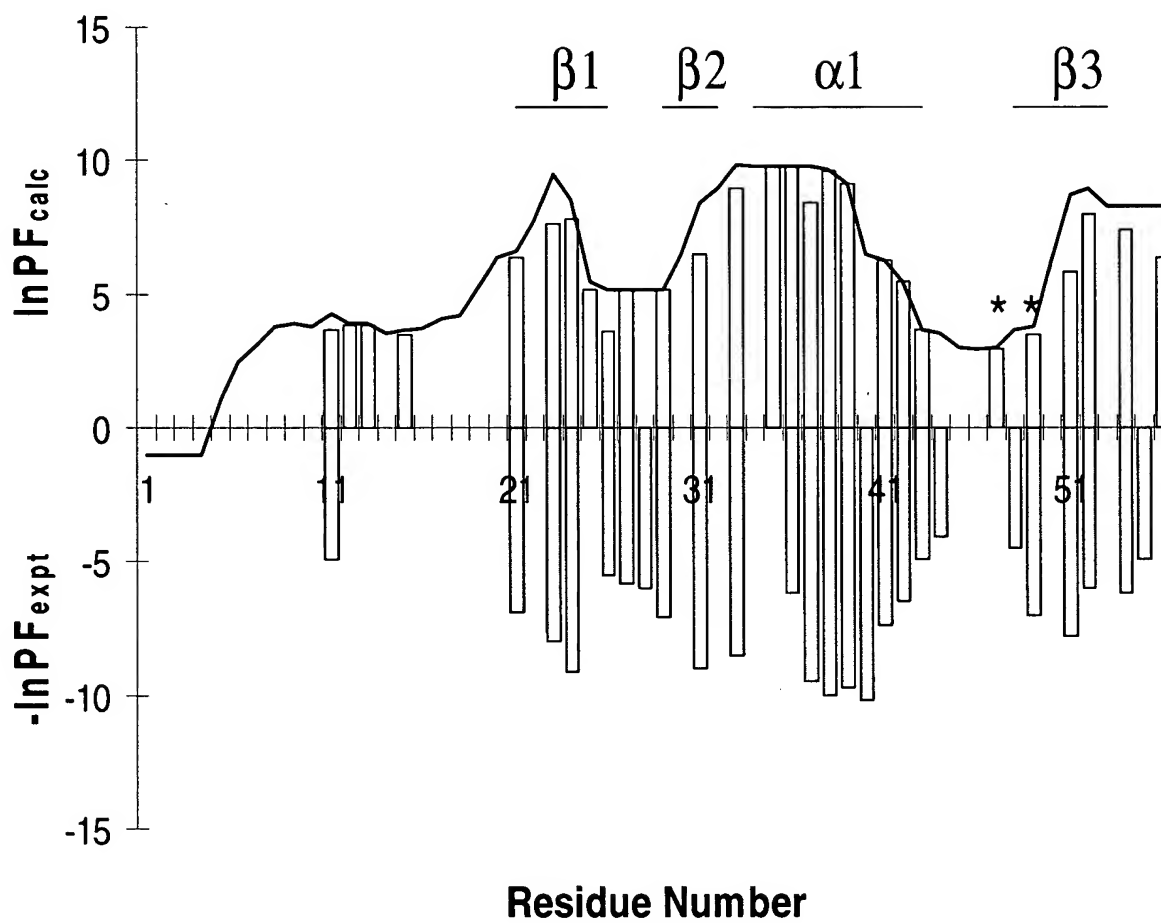
Asn 28

Lys 29

Thr 30

Figure 1

Figure 2
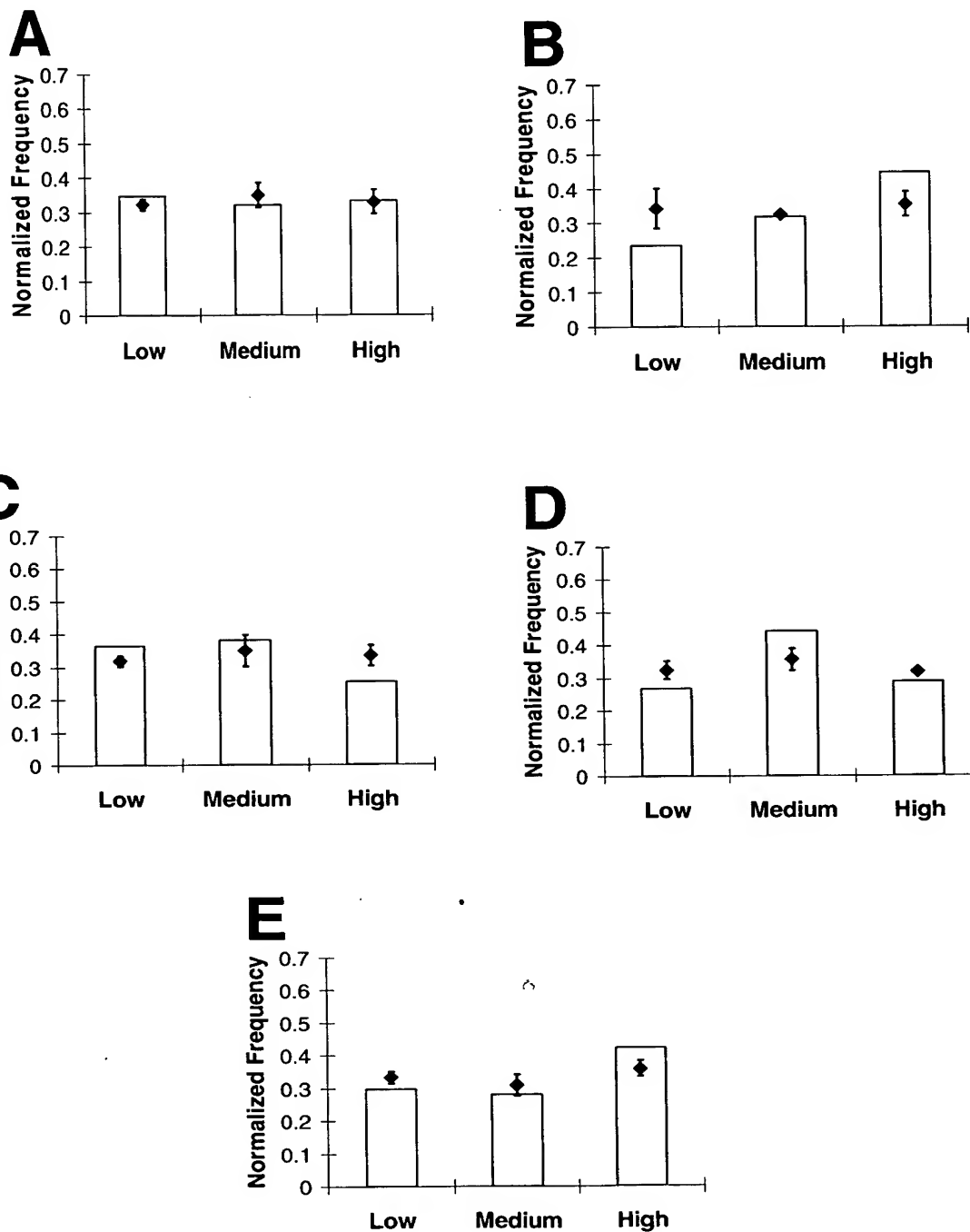
Figure 3

Figure 3
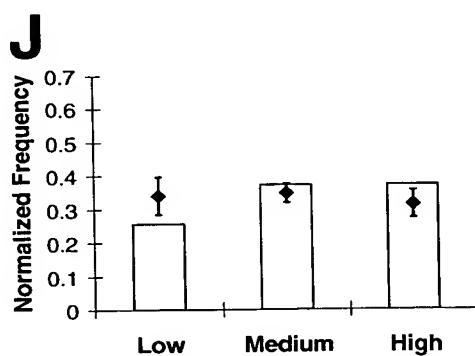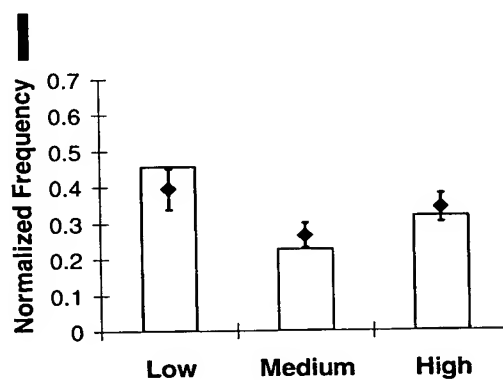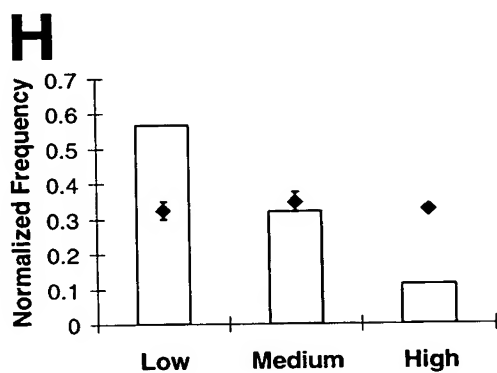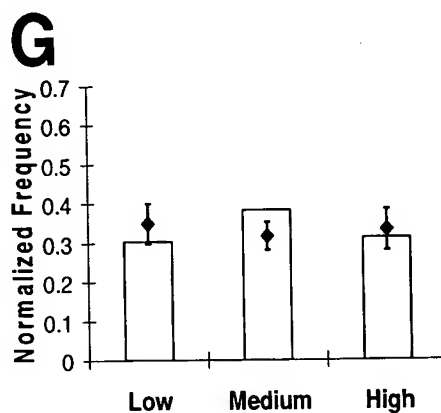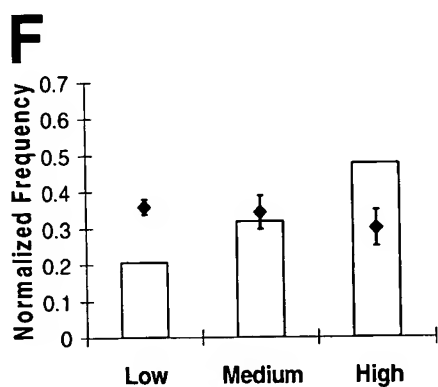
Figure 3
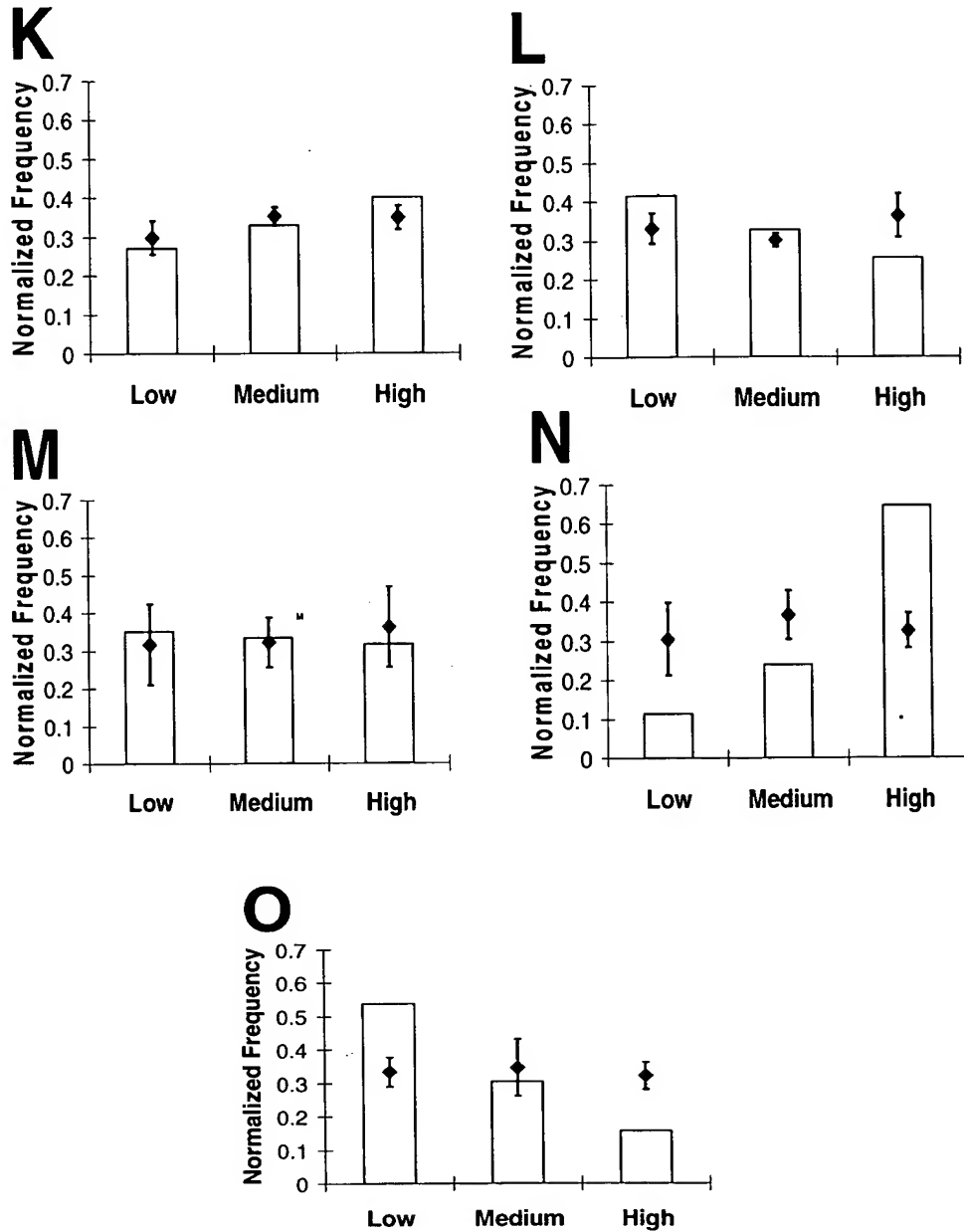
Figure 3

Figure 4
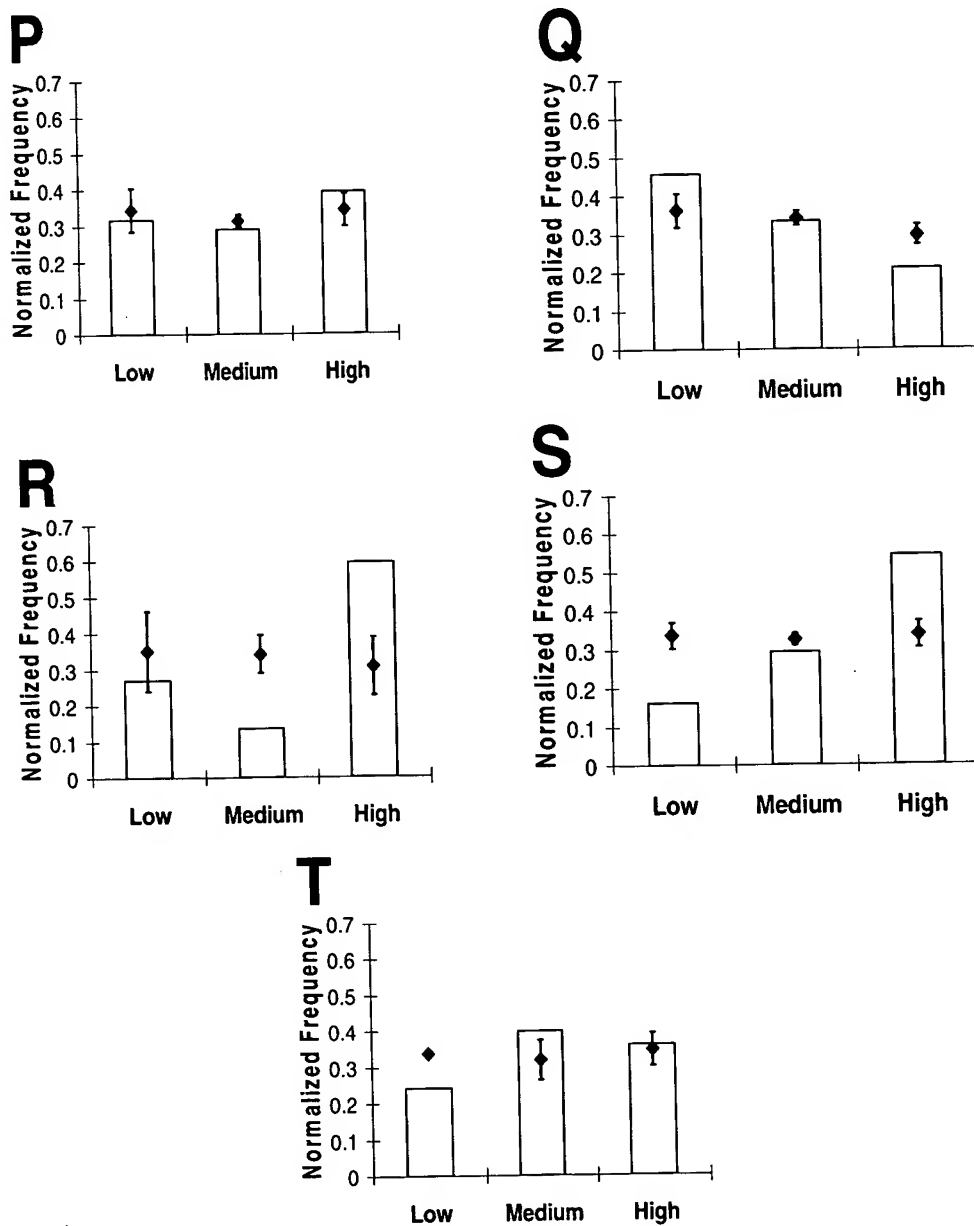
Figure 5A
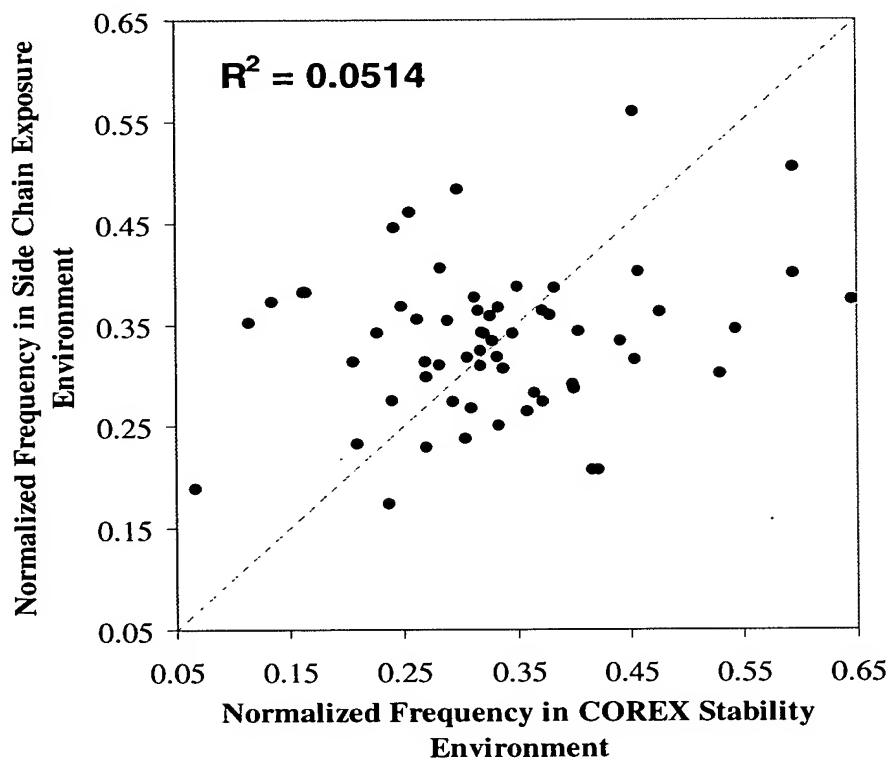
Figure 5B

Secondary Structure Scoring Matrix
Local Alignment Algorithm
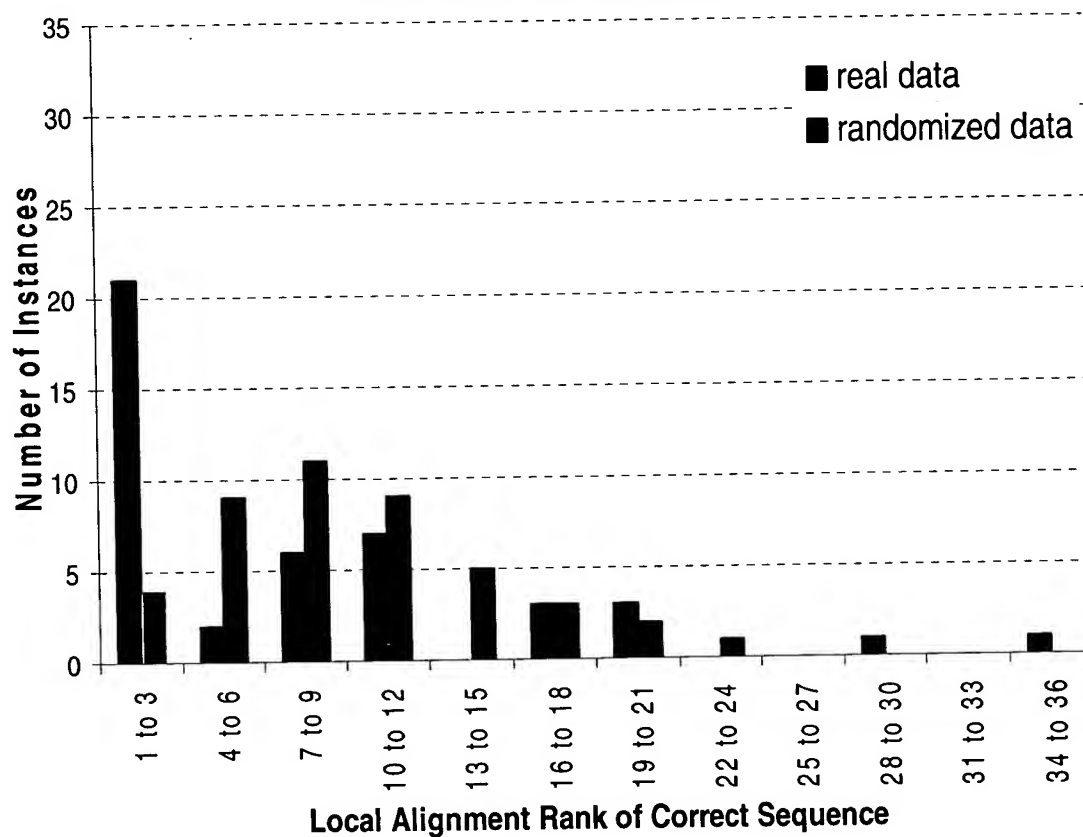
Figure 5

Secondary Structure Scoring Matrix
Global Alignment Algorithm
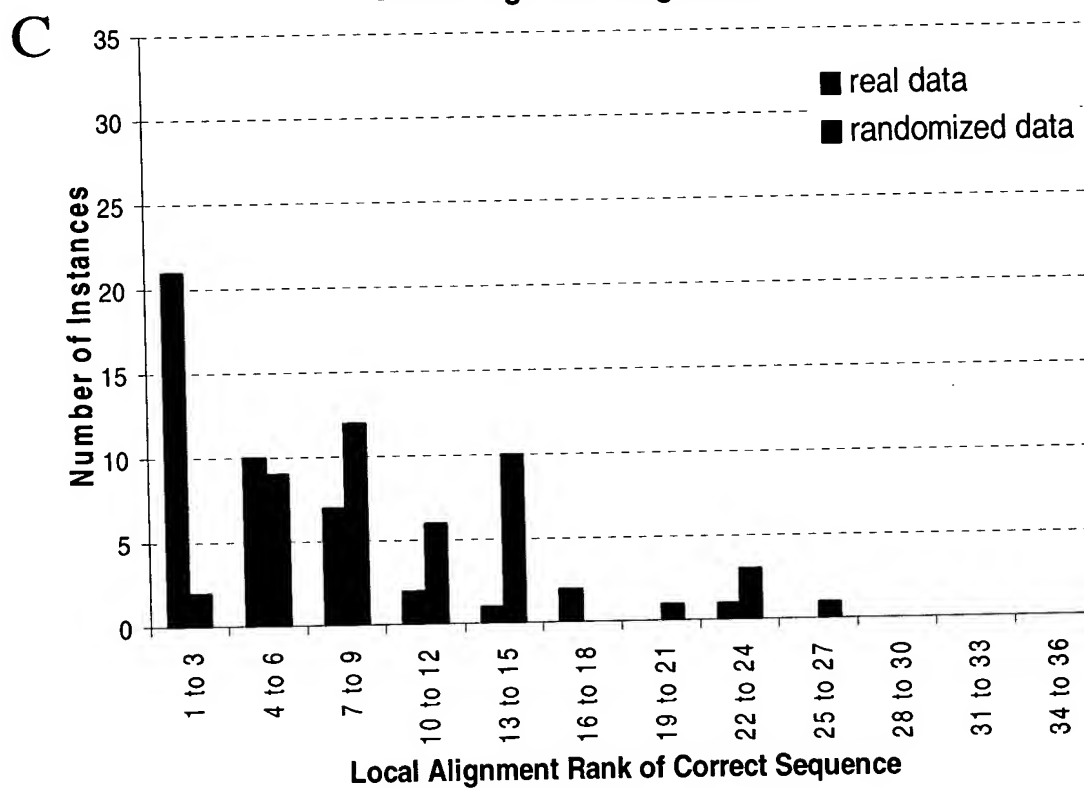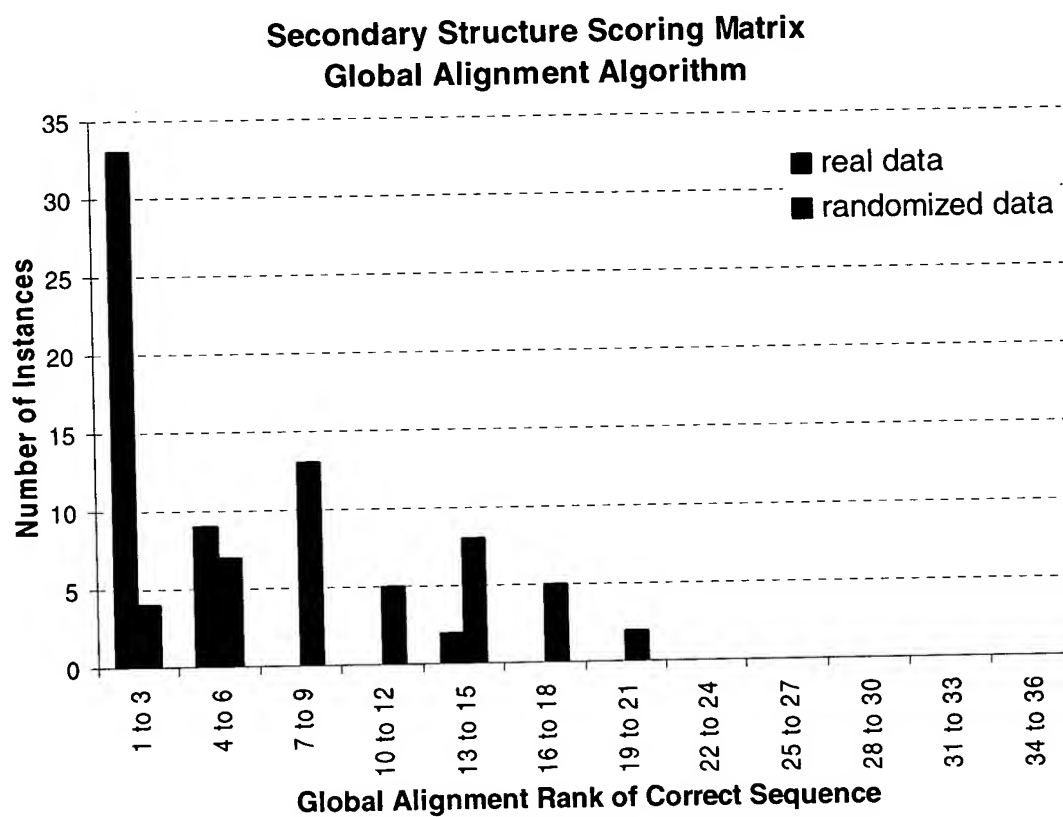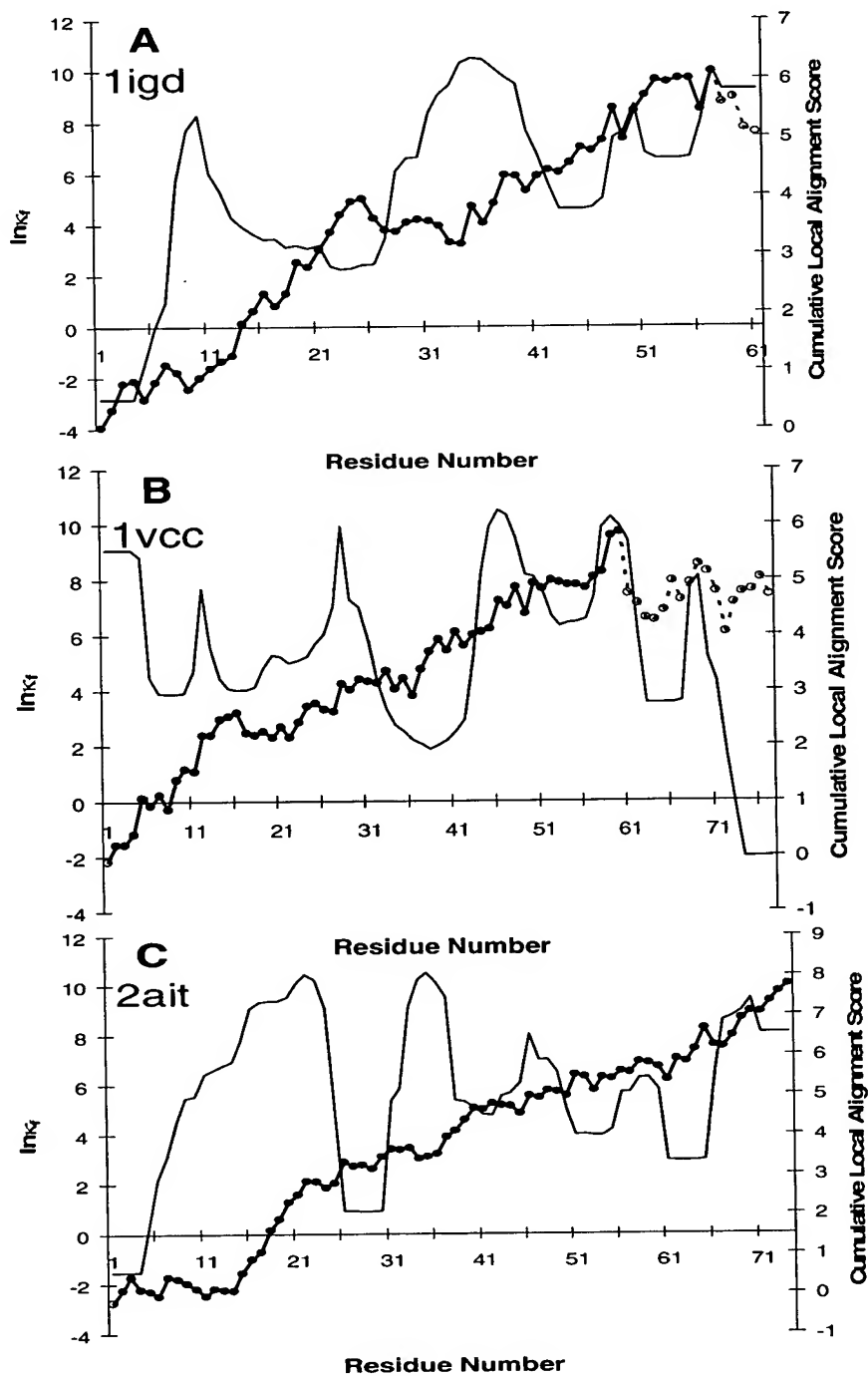
Figure 5

Figure 6

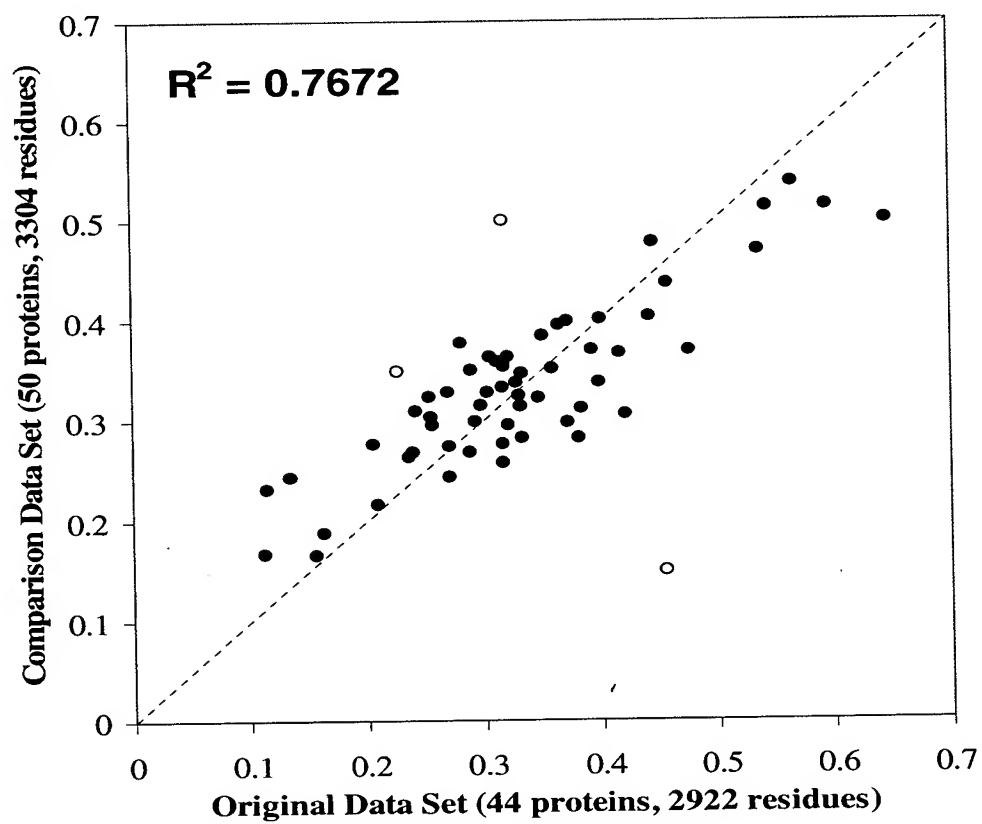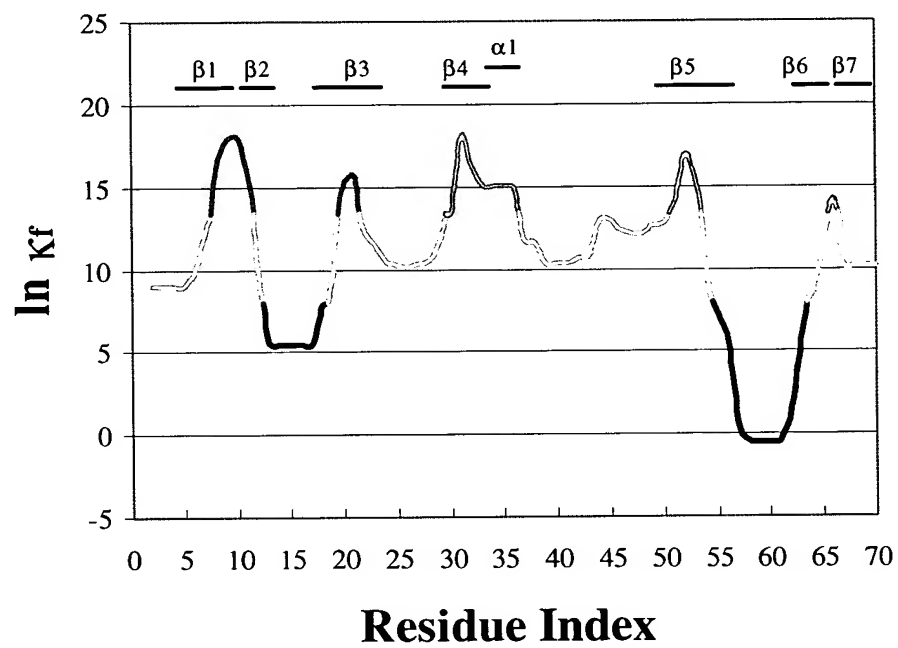Figure 7
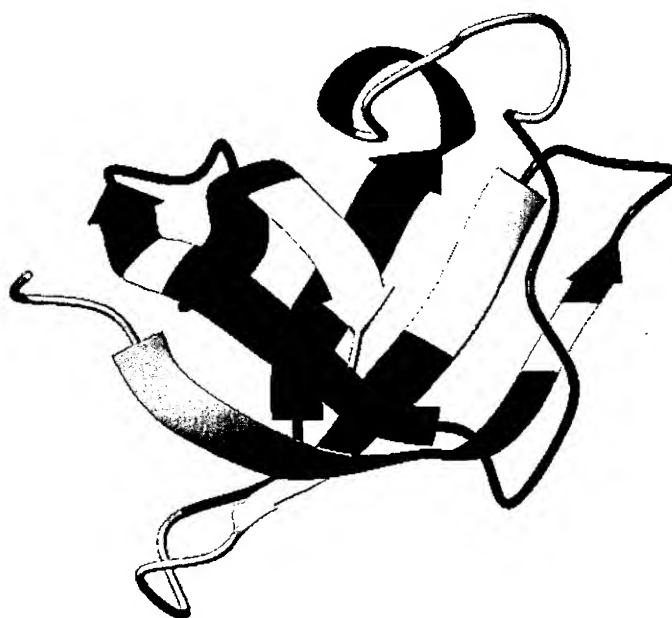
A

CspA (1MJC)

B

Figure 8

(a)

3 Stability Environments: Low (L), Medium (M), High (H)   **2 Enthalpy Environments:** Low (L), High (H)   **2 Entropy Environments:** Low (L), High (H)
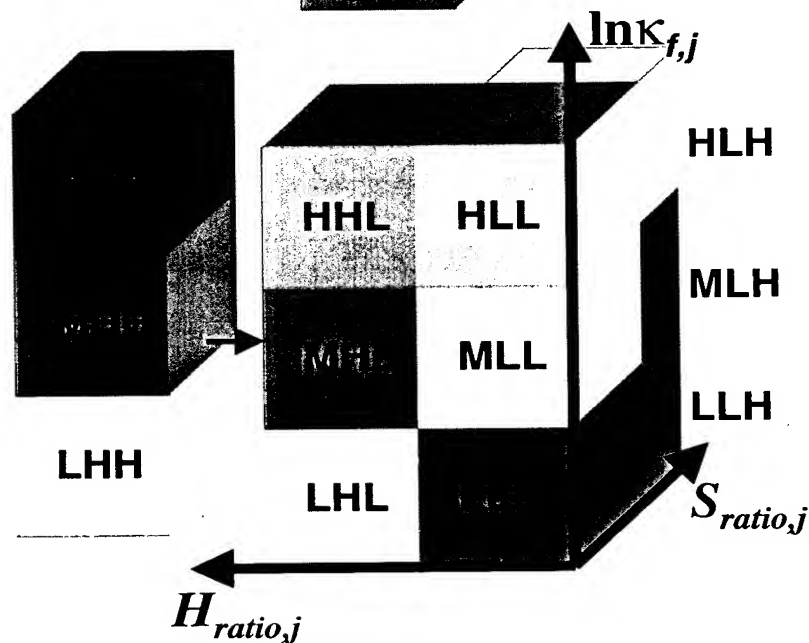
$$\kappa_{f,j} = \frac{\sum P_{f,j}}{\sum P_{nf,j}} \qquad H_{ratio,j} = \frac{\Delta H_{pol,j}}{\Delta H_{apol,j}} \qquad S_{ratio,j} = \frac{\Delta S_{conf,j}}{\Delta G_{solv,j}}$$

MHL

(b)

$\ln\kappa_{f,j}$

HLH

HHL HLL

MLH

MHL MLL

LLH

LHH

LHL

$S_{ratio,j}$

$H_{ratio,j}$
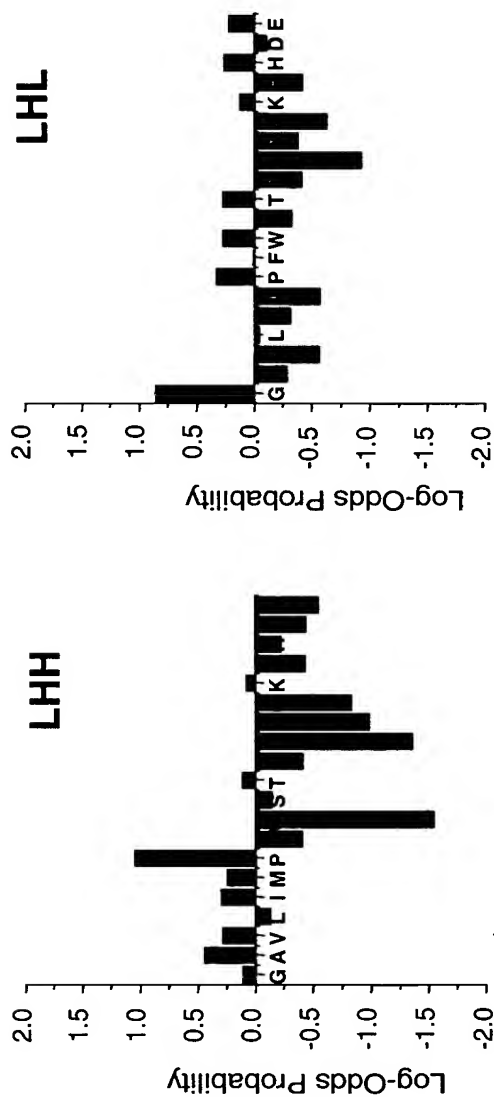
(c)

1HDJ:_
(All Alpha)

1PGB:_
(Alpha + Beta)

1SHG:_
(All Beta)

Figure 9

Figure 10A

Figure 10B
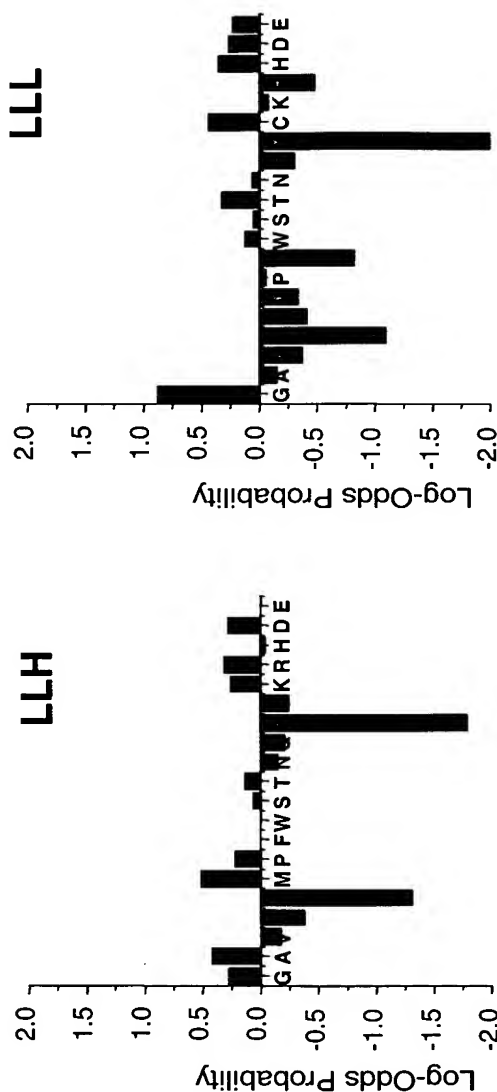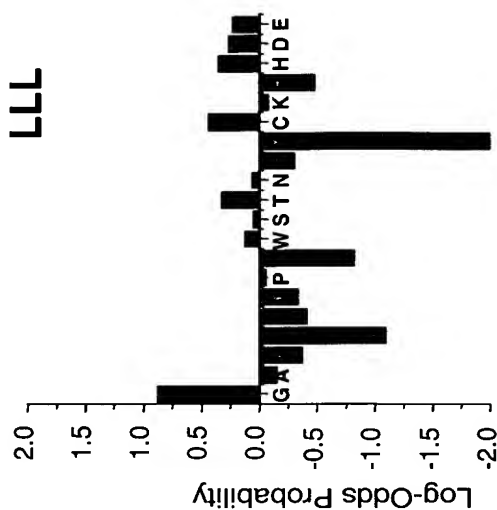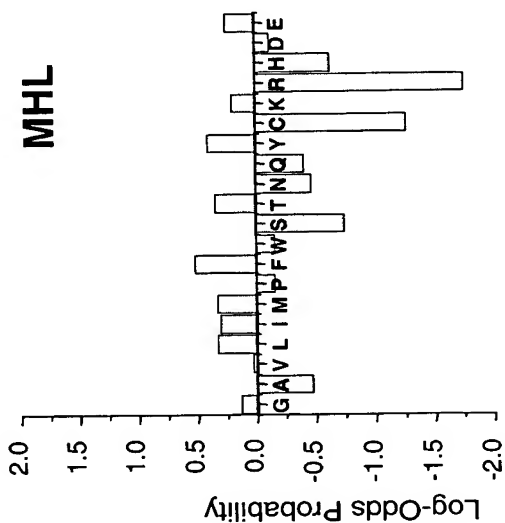
Figure 10C

Figure 10D
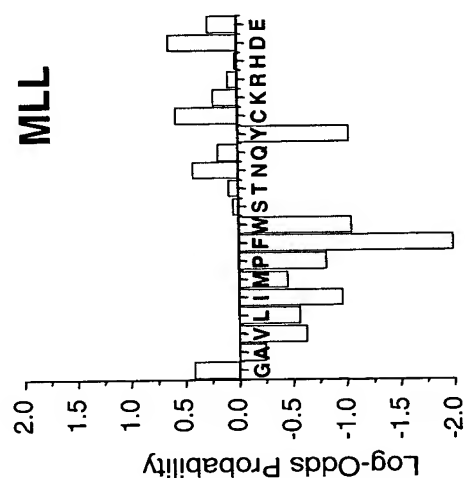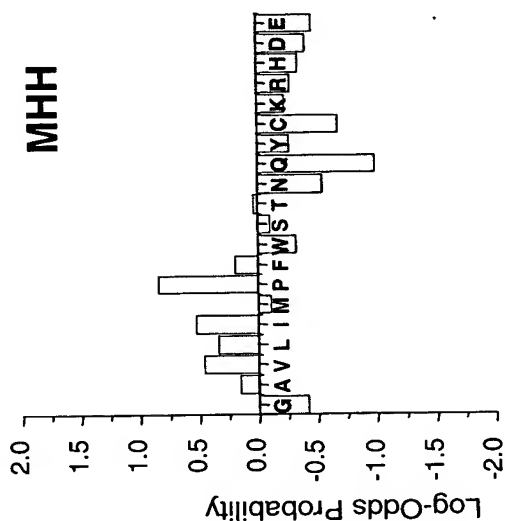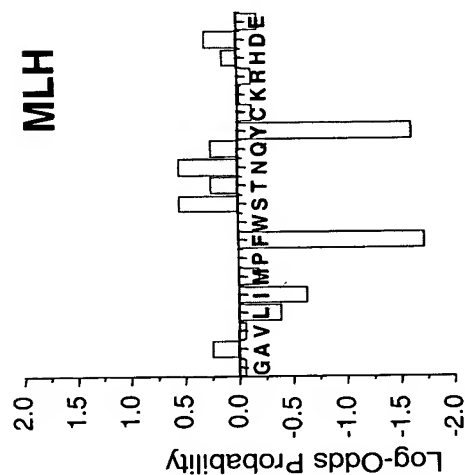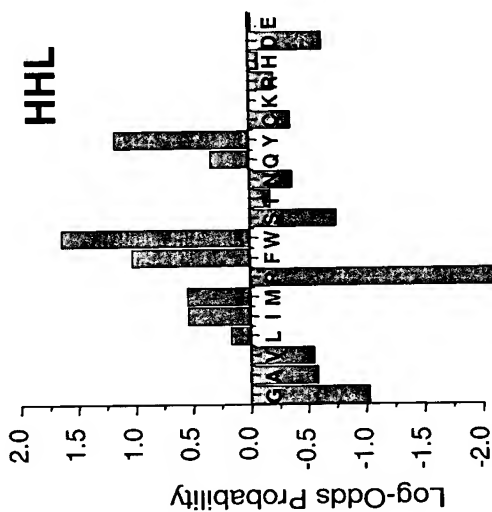
Figure 10F

Figure 10E

Figure 10H

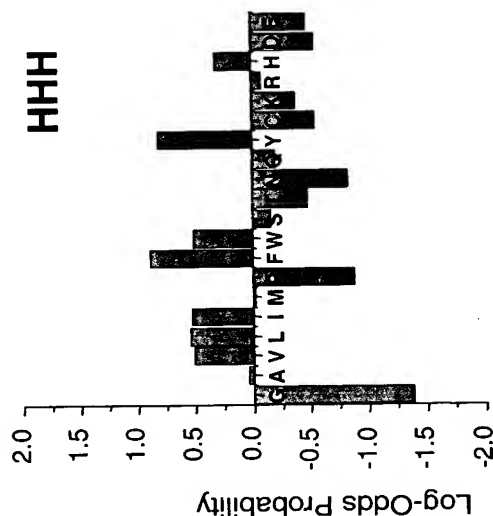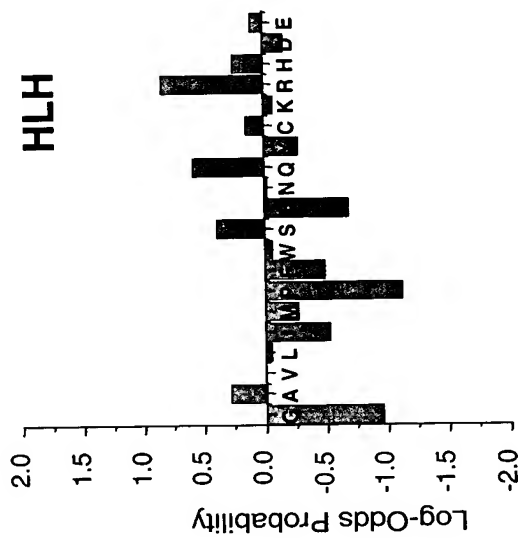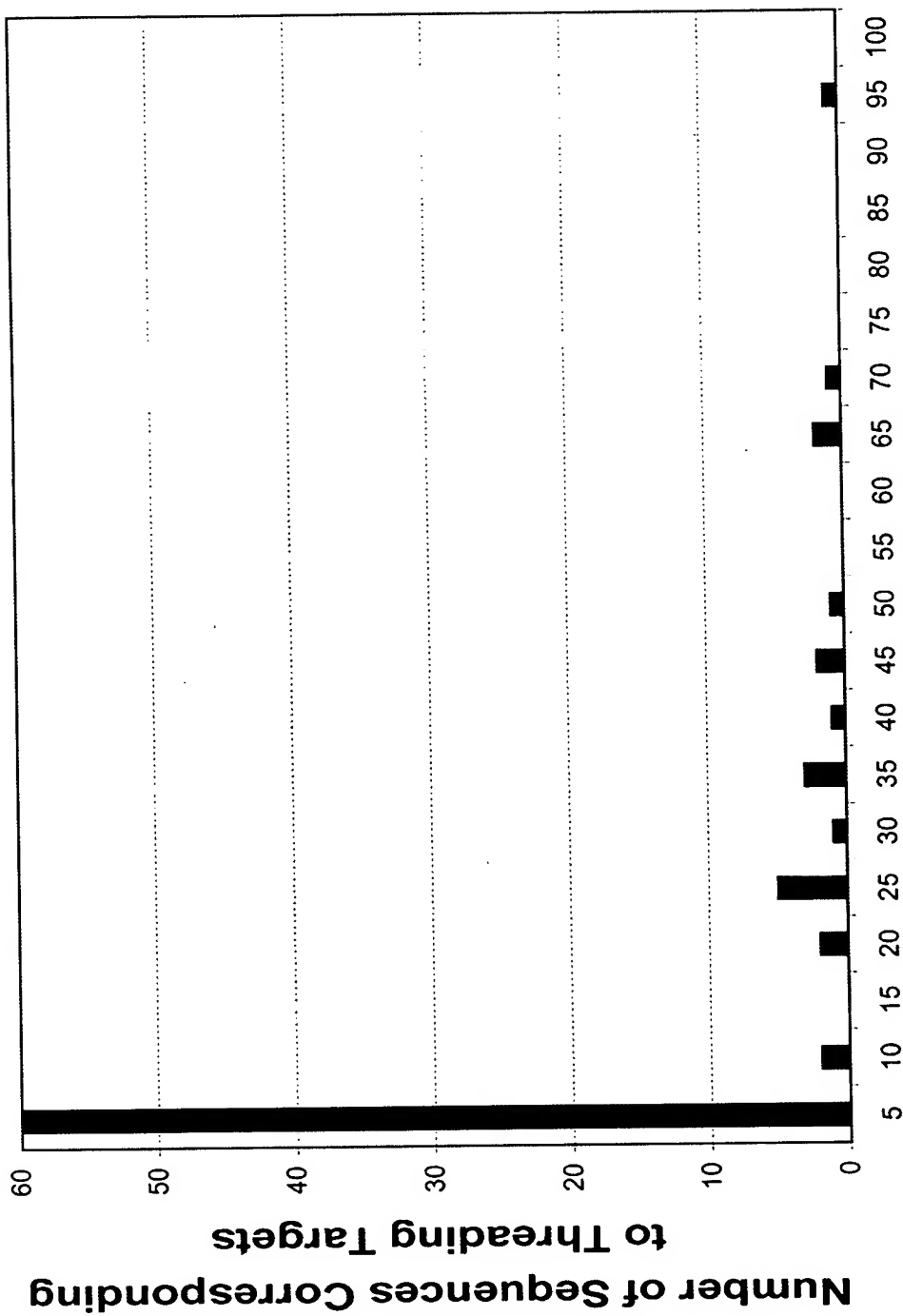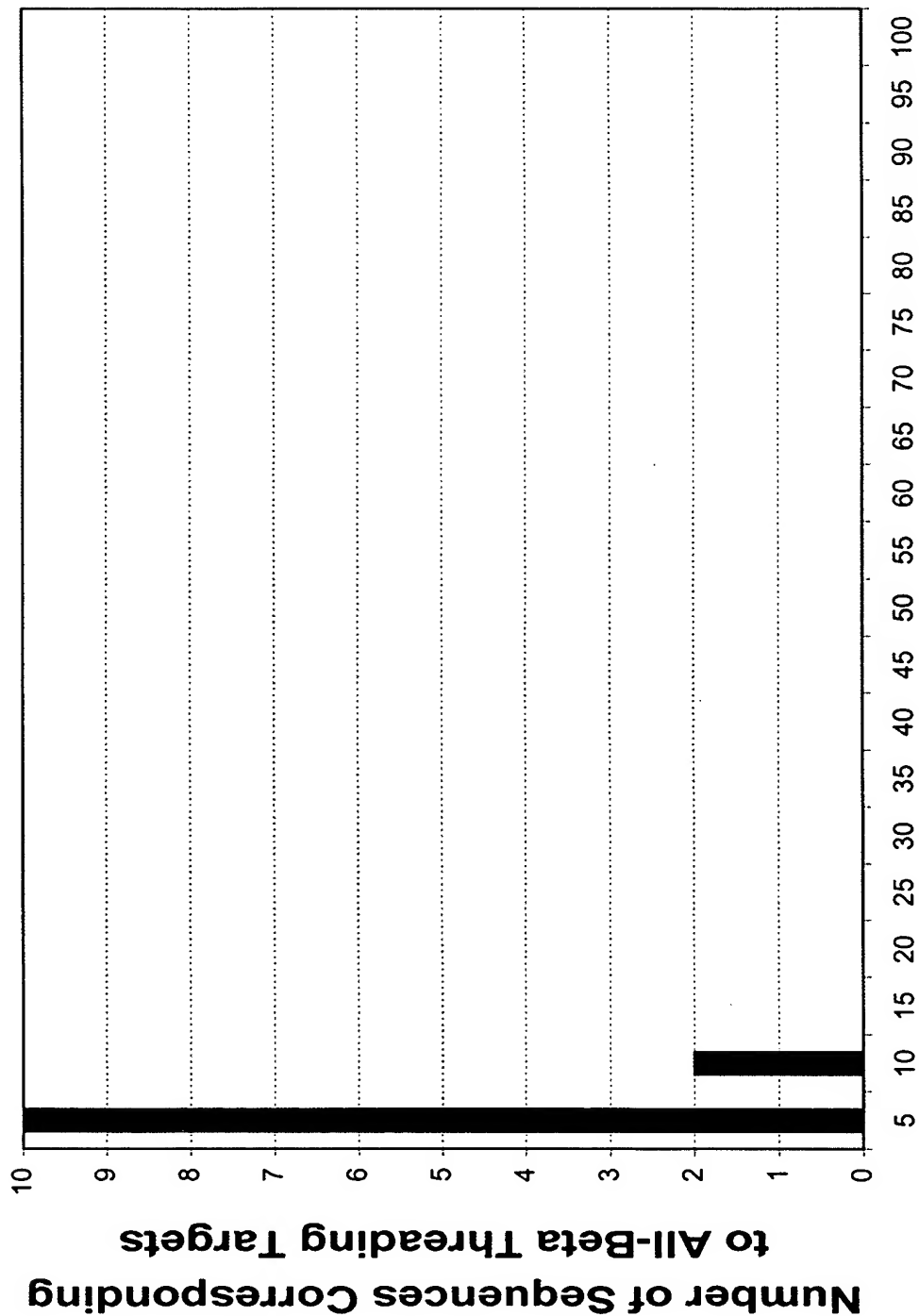Figure 10G
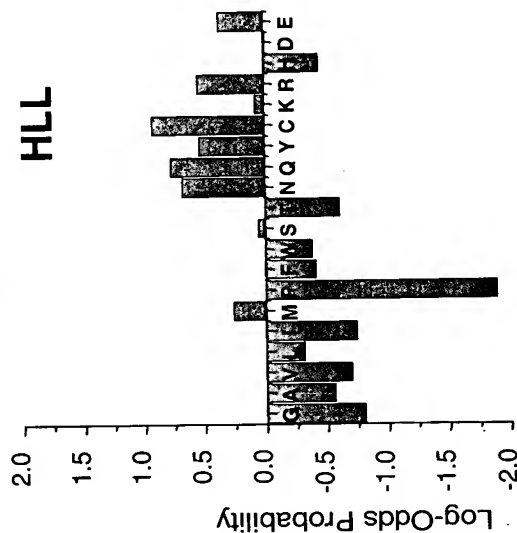
Figure 10I

Figure 10J

Figure 10K

Figure 10L

Percentile Rank of Sequence

Figure 11

Percentile Rank of Sequence

Figure 12

(Y-axis label: Number of Sequences Corresponding to All-Beta Threading Targets)